


Computational analysis

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 An abbreviated version of this protocol was published in Science Advances in Sep 2020

Diversification of reprogramming trajectories revealed by parallel single-cell transcriptome and chromatin accessibility sequencing

DOI: 10.1126/sciadv.aba1190

Related files

 1- Obtaining proper GTF for UCSC assemblies.doc	
 2- Creating a genome index for STAR mapper.doc	
 3- Quality Control of the fastq files.doc	
 4- Mapping RNA-Seq libraries using STAR (Fluidigm Libraries).doc	
 5- Gene Counting using Cuffquant (Fluidigm Libraries).doc	
 6- Obtaining normalized values using cuffnorm (Fluidigm Libraries).doc	
 7- Using Seurat for clustering the libraries using the FPKM table (Fluidigm Libraries).doc	
 8- Using RCA for clustering the libraries using the FPKM table (Fluidigm Libraries).doc	

How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. El Farran, C. (2021). Computational analysis. Bio-protocol Preprint. bio-protocol.org/prep957.
2. Xing, Q. R., Farran, C. A. E., Gautam, P., Chuah, Y. S., Warriar, T., Toh, C. X. D., Kang, N. Y., Sugii, S., Chang, Y. T., Xu, J., Collins, J. J., Daley, G. Q., Li, H., Zhang, L. F. and Loh, Y. H. (2020). Diversification of reprogramming trajectories revealed by parallel single-cell transcriptome and chromatin accessibility sequencing. Science Advances 6(37). DOI: [10.1126/sciadv.aba1190](https://doi.org/10.1126/sciadv.aba1190)

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